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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=31; hr=13; min=10; sec=55; ms=859;
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Application No: 10552786 Version No: 2.0

Input Set:**Output Set:**

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Finished: 2008-09-29 19:39:20.020
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Total Errors: 0
No. of SeqIDs Defined: 130
Actual SeqID Count: 130

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Input Set:

Output Set:

Started: 2008-09-29 19:39:18.196
Finished: 2008-09-29 19:39:20.020
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 824 ms
Total Warnings: 104
Total Errors: 0
No. of SeqIDs Defined: 130
Actual SeqID Count: 130

Error code

Error Description

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<110> DEPERTHES, David
CLOUTIER, Sylvain

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<141> 2006-07-25

<150> PCT/IB2004/001040

<151> 2004-04-05

<150> US 60/460345

<151> 2003-04-04

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<170> PatentIn version 3.5

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<211> 1239

<212> DNA

<213> Artificial sequence

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<223> DNA Sequence ACT variants : MD 820

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<213> Artificial sequence

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<223> Protein Sequence ACT variants : MD 820

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Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr
20 25 30

His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
35 40 45

Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
50 55 60

Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
65 70 75 80

His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
85 90 95

Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
100 105 110

Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn

115

120

125

Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
130 135 140

Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln
145 150 155 160

Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly
165 170 175

Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr
180 185 190

Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met
195 200 205

Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys
210 215 220

Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile
225 230 235 240

Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys
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Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys
260 265 270

Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp
275 280 285

Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys
290 295 300

Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu
305 310 315 320

Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr
325 330 335

Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu
340 345 350

Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys
355 360 365

Ile Thr Leu Arg Ser Arg Ala Val Glu Thr Arg Thr Ile Val Arg Phe
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405 410

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<211> 1239

<212> DNA

<213> Artificial sequence

<220>

<223> DNA Sequence ACT variant : MD 62

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aatgtcatct tctcccact gagcatctcc accgccttgg ctttctgtc tctgggggcc	240
cataatacca ccctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct	300
gaggcagaaa ttcaccagag cttccagcac ctctgcgc cactcaatca gtccagcgat	360
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gactcagctg cagctaagaa gctcatcaac gactacgtga agaattgaac tagggggaaa	540
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ttcttttaaag ccaaattgga gatgcccttt gacccccaag atactcatca gtcaagggtc	660
tacttgagca agaaaaagtg ggtaatgggtg cccatgatga gtttgcatca cctgactata	720
ccttacttcc gggacgagga gctgtcctgc accgtgggtg agctgaagta cacaggcaat	780
gccagcgcac tcttcatect ccctgatcaa gacaagatgg aggaagtgga agccatgctg	840
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 gcatctgctg ccaccgcggt caaaatcacc aggaggtcta tcgatgtgga gacgcgtacc 1140
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<213> Artificial sequence

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<223> Protein Sequence ACT variant : MD 62

<400> 4

Met Arg Gly Ser His His His His His Ser Arg His Pro Asn Ser
 1 5 10 15

Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr
 20 25 30

His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
 35 40 45

Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
 50 55 60

Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
 65 70 75 80

His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
 85 90 95

Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
 100 105 110

Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
 115 120 125

Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
 130 135 140

Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln
145 150 155 160

Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly
165 170 175

Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr
180 185 190

Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met
195 200 205

Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys
210 215 220

Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile
225 230 235 240

Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys
245 250 255

Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys
260 265 270

Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp
275 280 285

Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys
290 295 300

Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu
305 310 315 320

Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr
325 330 335

Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu
340 345 350

Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys
355 360 365

Ile Thr Arg Arg Ser Ile Asp Val Glu Thr Arg Thr Ile Val Arg Phe
 370 375 380

Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile
 385 390 395 400

Phe Phe Met Ser Lys Val Thr Asn Pro Lys Gln Ala
 405 410

<210> 5

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<213> Artificial sequence

<220>

<223> DNA Sequence ACT variant : MD 83

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aatgtcatct tctccccact gagcatctcc accgccttgg ccttcctgtc tctggggggcc	240
cataatacca ccctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct	300
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gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa	540
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ttcttttaaag ccaaattgga gatgcccttt gacccccaaag atactcatca gtcaaggttc	660
tacttgagca agaaaaagtg ggtaatgggtg cccatgatga gtttgcatca cctgactata	720
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<223> Protein Sequence ACT variant : MD 83

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20 25 30

His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
35 40 45

Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
50 55 60

Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
65 70 75 80

His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
85 90 95

Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
100 105 110

Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
115 120 125

Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
130 135 140

Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln
145 150 155 160

Asp	Ser	Ala	Ala	Ala	Lys	Lys	Leu	Ile	Asn	Asp	Tyr	Val	Lys	Asn	Gly	165	170	175	
Thr	Arg	Gly	Lys	Ile	Thr	Asp	Leu	Ile	Lys	Asp	Leu	Asp	Ser	Gln	Thr	180	185	190	
Met	Met	Val	Leu	Val	Asn	Tyr	Ile	Phe	Phe	Lys	Ala	Lys	Trp	Glu	Met	195	200	205	
Pro	Phe	Asp	Pro	Gln	Asp	Thr	His	Gln	Ser	Arg	Phe	Tyr	Leu	Ser	Lys	210	215	220	
Lys	Lys	Trp	Val	Met	Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	225	230	235	240
Pro	Tyr	Phe	Arg	Asp	Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	245	250	255	
Tyr	Thr	Gly	Asn	Ala	Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	260	265	270	
Met	Glu	Glu	Val	Glu	Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	275	280	285	
Arg	Asp	Ser	Leu	Glu	Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	290	295	300	
Phe	Ser	Ile	Ser	Arg	Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	305	310	315	320
Gly	Ile	Glu	Glu	Ala	Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	325	330	335	
Gly	Ala	Arg	Asn	Leu	Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	340	345	350	
Asp	Val	Phe	Glu	Glu	Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	355	360	365	
Ile	Arg	Gly	Arg	Ser	Glu	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	370	375	380	

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